



SEQUENCE LISTING

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<120> INHIBITORS OF STAPHYLOCOCCUS AUREUS PRIMARY SIGMA FACTOR AND USES THEREOF

<130> Q79408

<140> 10/771,395
<141> 2004-02-05

<150> US 60/445,441
<151> 2003-02-07

<160> 41

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Leu Thr Leu Glu Asp Val Lys Lys Gln Leu Ile Glu Lys Gly Lys Lys
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gag ggt cat tta agt cat gaa gaa att gct gaa aaa ctt cag aat ttt 144
Glu Gly His Leu Ser His Glu Glu Ile Ala Glu Lys Leu Gln Asn Phe
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gat atc gac tct gat caa atg gat gat ttc ttt gat caa tta aat gat 192
Asp Ile Asp Ser Asp Gln Met Asp Asp Phe Phe Asp Gln Leu Asn Asp
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Asn Asp Ile Ser Leu Val Asn Glu Lys Asp Ser Ser Asp Thr Asp Glu
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aaa ctg aat cca agt gat ctt agt gcc cct cca ggt gtt aaa ata aat 288

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Gln	Ala	Ile	Thr	Arg	Ala	Ile	Ala	Asp	Gln	Ala	Arg	Thr	Ile	Arg	Ile		
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Asp Ile Asp Ser Asp Gln Met Asp Asp Phe Phe Asp Gln Leu Asn Asp	
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Lys Leu Asn Pro Ser Asp Leu Ser Ala Pro Pro Gly Val Lys Ile Asn	
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Asp Pro Val Arg Met Tyr Leu Lys Glu Ile Gly Arg Val Asn Leu Leu	
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115 120 125	

Glu Val Ala Lys Ser Arg Leu Ala Glu Ala Asn Leu Arg Leu Val Val
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Ser Ile Ala Lys Arg Tyr Val Gly Arg Gly Met Leu Phe Leu Asp Leu
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Ile Gln Glu Gly Asn Met Gly Leu Ile Lys Ala Val Glu Lys Phe Asp
165 170 175

Phe Asn Lys Gly Phe Lys Phe Ser Thr Tyr Ala Thr Trp Trp Ile Arg
180 185 190

Gln Ala Ile Thr Arg Ala Ile Ala Asp Gln Ala Arg Thr Ile Arg Ile
195 200 205

Pro Val His Met Val Glu Thr Ile Asn Lys Leu Ile Arg Val Gln Arg
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Gln Leu Leu Gln Asp Leu Gly Arg Asp Pro Ala Pro Glu Glu Ile Gly
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Glu Glu Met Asp Leu Pro Ala Glu Lys Val Arg Glu Ile Leu Lys Ile
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Ala Gln Glu Pro Val Ser Leu Glu Thr Pro Ile Gly Glu Glu Asp Asp
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Ser His Leu Gly Asp Phe Ile Glu Asp Gln Glu Ala Gln Ser Pro Ser
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305 310 315 320

Leu Asp Asp Gly Arg Thr Arg Thr Leu Glu Glu Val Gly Lys Val Phe
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Phe Asp Phe Asn Lys Gly Phe Lys Phe Ser Thr Tyr Ala Thr Trp Trp
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Gln Arg Gln Leu Leu Gln Asp Leu Gly Arg Asp Pro Ala Pro Glu Glu
 100 105 110

Ile Gly Glu Glu Met Asp Leu Pro Ala Glu Lys Val Arg Glu Ile Leu
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Lys Ile Ala Gln Glu Pro Val Ser Leu Glu Thr Pro Ile Gly Glu Glu
 130 135 140

Asp Asp Ser His Leu Gly Asp Phe Ile Glu Asp Gln Glu Ala Gln Ser
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 165 170 175

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Phe Gly Leu Asp Asp Gly Arg Thr Arg Thr Leu Glu Glu Val Gly Lys
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Thr Arg Thr Leu Glu Glu Val Gly Lys Val Phe Gly Val Thr Arg Glu
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 His Arg Asn Lys Glu His Lys Thr Ile Asp Asn Val Pro Thr Ala Asn
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 35 40 45
 aga aac ggg gaa tac tta gaa tta aaa aga tta cgt tct act tta cct 192
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 50 55 60
 tca tct tat ggt tta gat gat aat aac caa gat att att aga gat aat 240
 Ser Ser Tyr Gly Leu Asp Asp Asn Asn Gln Asp Ile Ile Arg Asp Asn
 65 70 75 80
 aac cat aga tgt aaa ata ggt tat tgg tac aac cct gca gta cgc aaa 288
 Asn His Arg Cys Lys Ile Gly Tyr Trp Tyr Asn Pro Ala Val Arg Lys
 85 90 95
 gat aat tta aag att ata gag aaa gct aaa caa tat gga tta cct att 336
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 100 105 110

ata aca gaa gaa tat gat gct aat act gta gag caa gga ttt aga gat	384
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cta gaa ggt aaa aca gaa gaa gaa tta aga ata ttt aac atg aaa tca	480
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165 170 175	
gat tta act tat agt gac tta gga caa att tat aat atg ttg tta tta	576
Asp Leu Thr Tyr Ser Asp Leu Gly Gln Ile Tyr Asn Met Leu Leu Leu	
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Ser Ser Tyr Gly Leu Asp Asp Asn Asn Gln Asp Ile Ile Arg Asp Asn	
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100 105 110

Ile Thr Glu Glu Tyr Asp Ala Asn Thr Val Glu Gln Gly Phe Arg Asp
115 120 125

Ile Gly Val Ile Phe Gln Ser Leu Lys Thr Ile Val Val Thr Arg Tyr
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Leu Glu Gly Lys Thr Glu Glu Glu Leu Arg Ile Phe Asn Met Lys Ser
145 150 155 160

Glu Glu Ser Gln Leu Asn Glu Ala Leu Lys Glu Ser Asp Phe Ser Val
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His Arg Cys Lys Ile Gly Tyr Trp Tyr Asn Pro Ala Val Arg Lys Asp
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Asn Leu Lys Ile Ile Glu Lys Ala Lys Gln Tyr Gly Leu Pro Ile Ile
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Thr Glu Glu Tyr Asp Ala Asn Thr Val Glu Gln Gly Phe Arg Asp Ile
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Gly Val Ile Phe Gln Ser Leu Lys Thr Ile Val Val Thr Arg Tyr Leu
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Glu Gly Lys Thr Glu Glu Glu Leu Arg Ile Phe Asn Met Lys Ser Glu
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Glu Ser Gln Leu Asn Glu Ala Leu Lys Glu Ser Asp Phe Ser Val Asp
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Asn Ser Met Gly Val Thr Lys Leu Asp Val Pro Leu Ser Asn Ile His
20 25 30
gaa tgg tat cct ttt tct aac gct tat tct tac aag tat aat gta aaa 144
Glu Trp Tyr Pro Phe Ser Asn Ala Tyr Ser Tyr Lys Tyr Asn Val Lys
35 40 45
aca aaa gat tta gta tta aaa cga cta cgt tca tca cta cca gta tct 192
Thr Lys Asp Leu Val Leu Lys Arg Leu Arg Ser Ser Leu Pro Val Ser
50 55 60
tat ggg att gaa cga gcg tct aaa gag tat gac aaa gat aaa gta tgt 240
Tyr Gly Ile Glu Arg Ala Ser Lys Glu Tyr Asp Lys Asp Lys Val Cys
65 70 75 80
aac aca gta aca tgg ata aac cat tca gta aaa gac agt aat tta cac 288
Asn Thr Val Thr Trp Ile Asn His Ser Val Lys Asp Ser Asn Leu His
85 90 95
att att aat aaa gct aaa tca tat ggg tta cct gtt att aca gaa aag 336
10/36

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ttt	tct	gaa	tta	aaa	tct	ttg	att	att	aat	cgt	tat	tta	gag	gat	aaa	432
Phe	Ser	Glu	Leu	Lys	Ser	Leu	Ile	Ile	Asn	Arg	Tyr	Leu	Glu	Asp	Lys	
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Asp	Gly	Ser	Phe	Ile	Val	Lys	Phe	Lys	Arg	His	Asn	Pro	Glu	Thr	Gln	
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Tyr	His	Leu	Ala	Val	Gln	Asp	Ala	Asp	Glu	Val	Ile	Asn	Asn	Thr	Tyr	
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gat	gag	cta	ggg	caa	atg	tat	aaa	atg	tta	tta	cta	atg	aag	aaa	tta	576
Asp	Glu	Leu	Gly	Gln	Met	Tyr	Lys	Met	Leu	Leu	Leu	Met	Lys	Lys	Leu	
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95

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Tyr His Leu Ala Val Gln Asp Ala Asp Glu Val Ile Asn Asn Thr Tyr
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 35 40 45

Xaa Xaa Xaa Leu Xaa Leu Lys Arg Leu Arg Ser Xaa Leu Pro Xaa Ser
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Tyr Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Cys
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Xaa Xaa Xaa Xaa Trp Xaa Asn Xaa Xaa Val Xaa Xaa Xaa Asn Leu Xaa
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Ile Ile Xaa Lys Ala Lys Xaa Tyr Gly Leu Pro Xaa Ile Thr Glu Xaa
 29/36

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 <400> 35
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 <210> 36
 <211> 34
 <212> DNA
 <213> artificial sequence

 <220>
 <223> Chemically synthesized PCR primer

 <400> 36
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 <210> 37
 <211> 30
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 <213> artificial sequence

 <220>
 <223> Chemically synthesized probe

 <400> 37
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 <210> 38
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 <400> 38

accaattttta ttcaataagt caatatcat 29

<210> 39
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<220>
<223> Chemically synthesized probe

<400> 39
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<210> 40
<211> 48
<212> DNA
<213> artificial sequence

<220>
<223> Chemically synthesized oligonucleotide competitor sequence

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<210> 41
<211> 49
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<220>
<223> Chemically synthesized oligonucleotide competitor sequence

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